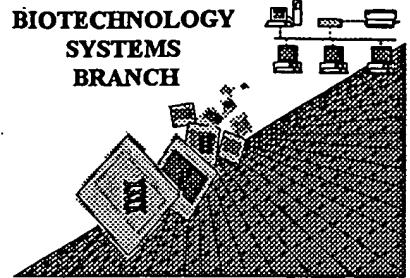


Saunders

RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/121,017

Art Unit / Team No.: 1644

Date Processed by STIC: 12/17/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/121,017</u>
TN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
— Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
— Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
— Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
— Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
— Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
— Variable Length	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
— PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.	
— Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
— Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
— Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
— Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response. <i>135 (maybe more)</i>	
— Use of <220>Feature (NEW RULES)	Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
— PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/121,017DATE: 12/17/1999
TIME: 16:20:58

Input Set: I121017.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Imamura, Toru
 2 Asada, Masahiro
 3 Oka, Syuichi
 4 Suzuki, Masashi
 5 Yoneda, Atsuko
 6 Ota, Keiko
 7 Oda, Yuko
 8 Miyakawa, Kazuko
 9 Orikasa, Noriko
 10 Asada, Chie
 11 Kojima, Tetsuhito
 12 <120> TITLE OF INVENTION: HEPARIN-BINDING PROTEINS MODIFIED WITH SUGAR CHAINS,
 13 METHOD OF PRODUCING THE SAME AND PHARMACEUTICAL
 14 COMPOSITIONS CONTAINING THE SAME
 15 <130> FILE REFERENCE: PH-559US
 16 <140> CURRENT APPLICATION NUMBER: US/09/121,017
 17 <141> CURRENT FILING DATE: 1998-07-23
 18 <150> EARLIER APPLICATION NUMBER: 307721/1997
 19 <151> EARLIER FILING DATE: 1997-11-10
 20 <160> NUMBER OF SEQ ID NOS: 30
 21 <170> SOFTWARE: PatentIn Ver. 2.0
 22 <210> SEQ ID NO 1
 23 <211> LENGTH: 221
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Artificial Sequence
 26 <400> SEQUENCE: 1

See item 12 on Error Summary Sheet

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Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
      20          25          30
Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
      35          40          45
Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
      50          55          60
Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
      65          70          75          80
Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
      85          90          95
Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
      100         105         110
Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
      115         120         125
Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
      130         135         140
  
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RAW SEQUENCE LISTING
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Input Set: I121017.RAW

45 Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
 46 145 150 155 160
 47 Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
 48 165 170 175
 49 Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
 50 180 185 190
 51 Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
 52 195 200 205
 53 Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
 54 210 215 220
 55 <210> SEQ ID NO 2
 56 <211> LENGTH: 663
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Artificial Sequence
 59 <220> FEATURE:
 60 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
 61 sequence for a part of human rydocal and a part of human fibroblast
 62 growth factor 1
 63 <220> FEATURE:
 64 <221> NAME/KEY: CDS
 65 <222> LOCATION: (1)..(663)
 66 <400> SEQUENCE: 2
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 69 1 5 10 15
 gtc gcc gag tcg atc cga gag act gag gtc atc gac ccc cag gac ctc 96
 Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
 72 20 25 30
 cta gaa ggc cga tac ttc tcc gga gcc cta cca gac gat gag gat gta 144
 Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
 74 35 40 45
 gtg ggg ccc ggg cag gaa tct gat gac ttt gag ctg tct ggc tct gga 192
 Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
 77 50 55 60
 gat ctg gat gac ttg gaa gac tcc atg atc ggc cct gaa gtt gtc cat 240
 Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
 80 65 70 75 80
 ccc ttg gtg cct cta gat gct aat tac aag aag ccc aaa ctc ctc tac 288
 Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
 83 85 90 95
 tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc aca gtg 336
 Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
 86 100 105 110
 gat ggg aca agg gac agg agc gac cag cac att cag ctg cag ctc agt 384
 Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
 89 115 120 125
 gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act ggc cag 432
 Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
 92 130 135 140
 tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag aca cca 480

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95      Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
96          145           150           155           160
97      aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag aac cat tac aac  528
98      Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
99          165           170           175
100     acc tat ata tcc aag aag cat gca gag aag aat tgg ttt gtt ggc ctc  576
101     Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
102          180           185           190
103     aag aag aat ggg agc tgc aaa cgc ggt cct cgg act cac tat ggc cag  624
104     Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
105          195           200           205
106     aaa gca atc ttg ttt ctc ccc ctg cca gtc tct tct gat  663
107     Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
108          210           215           220
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110 <211> LENGTH: 175
111 <212> TYPE: PRT
112 <213> ORGANISM: Artificial Sequence
113 <400> SEQUENCE: 3
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116      Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
117          20          25          30
118      Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
119          35          40          45
120      Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
121          50          55          60
122      Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
123          65          70          75          80
124      Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
125          85          90          95
126      Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
127          100         105         110
128      Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His
129          115         120         125
130      Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val
131          130         135         140
132      Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr
133          145         150         155         160
134      Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
135          165         170         175
136 <210> SEQ ID NO 4
137 <211> LENGTH: 525
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
140 <220> FEATURE:
141 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
142 sequence for a part of mouse fibroblast growth factor 6 and
143 a part of human fibroblast growth factor 1
144 <220> FEATURE:

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/121,017

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Input Set: I121017.RAW

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145 <221> NAME/KEY: CDS
146 <222> LOCATION: (1)..(525)
147 <400> SEQUENCE: 4
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150         1           5           10          15
151     ttc tta ggc gtc cta gtg ggc atg gtg gtg ccc tca cct gcc ggc gcc 96
152     Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
153         20          25          30
154     cgc gcc aac ggc acg cta ctg gac gct aat tac aag aag ccc aaa ctc 144
155     Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
156         35          40          45
157     ctc tac tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc 192
158     Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
159         50          55          60
160     aca gtg gat ggg aca agg gac agg agc gac cag cac att cag ctg cag 240
161     Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
162         65          70          75          80
163     ctc agt gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act 288
164     Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
165         85          90          95
166     ggc cag tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag 336
167     Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
168         100         105         110
169     aca cca aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag aac cat 384
170     Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His
171         115         120         125
172     tac aac acc tat ata tcc aag aag cat gca gag aag aat tgg ttt gtt 432
173     Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val
174         130         135         140
175     ggc ctc aag aat ggg agc tgc aaa cgc ggt cct ccg act cac tat 480
176     Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr
177         145         150         155         160
178     ggc cag aaa gca atc ttg ttt ctc ccc ctg cca gtc tct tct gat 525
179     Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
180         165         170         175
181 <210> SEQ ID NO 5
182 <211> LENGTH: 181
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
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189         20          25          30
190     Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
191         35          40          45
192     Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
193         50          55          60
194     Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln

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195 65 70 75 80
 196 Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
 197 85 90 95
 198 Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
 199 100 105 110
 200 Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Ala Ala
 201 115 120 125
 202 Thr Pro Ala Pro Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala
 203 130 135 140
 204 Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg
 205 145 150 155 160
 206 Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu
 207 165 170 175
 208 Pro Val Ser Ser Asp
 209 180
 210 <210> SEQ ID NO 6
 211 <211> LENGTH: 543
 212 <212> TYPE: DNA
 213 <213> ORGANISM: Artificial Sequence
 214 <220> FEATURE:
 215 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
 216 sequence for a part of mouse fibroblast growth factor 6,
 217 a part of human fibroblast growth factor 1 and an artificial
 218 sequence
 219 <220> FEATURE:
 220 <221> NAME/KEY: CDS
 221 <222> LOCATION: (1)..(543)
 222 <400> SEQUENCE: 6

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225 1 5 10 15	
226 ttc tta ggc gtc cta gtg ggc atg gtg gtg ccc tca cct gcc ggc gcc	96
227 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala	
228 20 25 30	
229 cgc gcc caa ggc acg cta ctg gac gct aat tac aag aag ccc aaa ctc	144
230 Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu	
231 35 40 45	
232 ctc tac tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc	192
233 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly	
234 50 55 60	
235 aca gtg gat ggg aca agg gac agg agc gac cag cac att cag ctg cag	240
236 Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln	
237 65 70 75 80	
238 ctc agt gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act	288
239 Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr	
240 85 90 95	
241 ggc cag tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag	336
242 Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln	
243 100 105 110	
244 aca cca aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag gct gct	384

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/121,017

DATE: 12/17/1999
TIME: 16:20:58

Input Set: I121017.RAW

Line ? Error/Warning

Original Text
